E. Coli

Fig. 1a

Bacillus Subtilis

Fig. 1b

Archaeglobus fulgidus

Position
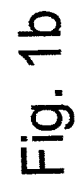
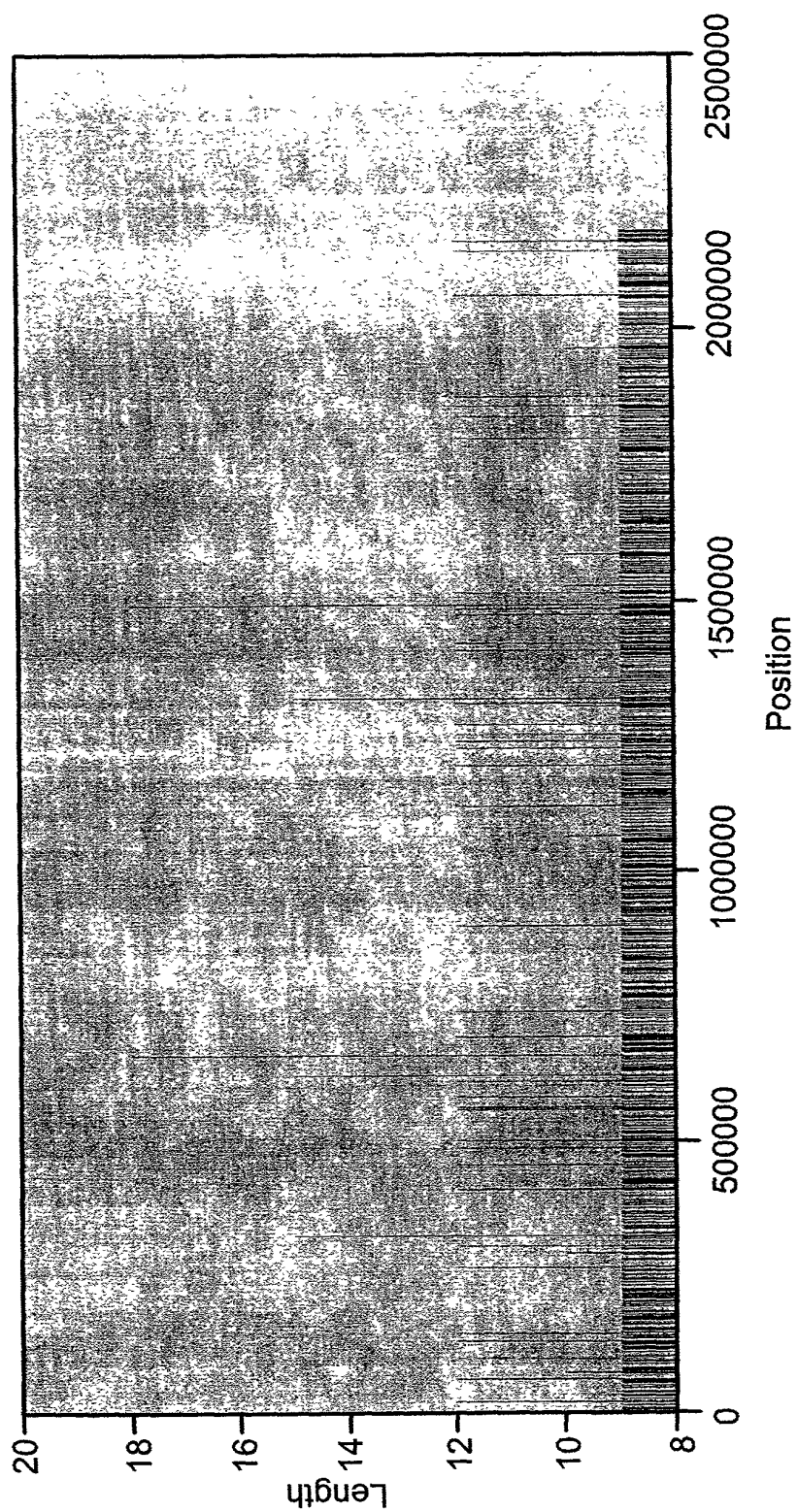Fig. 1c

Yeast Chromosome 7
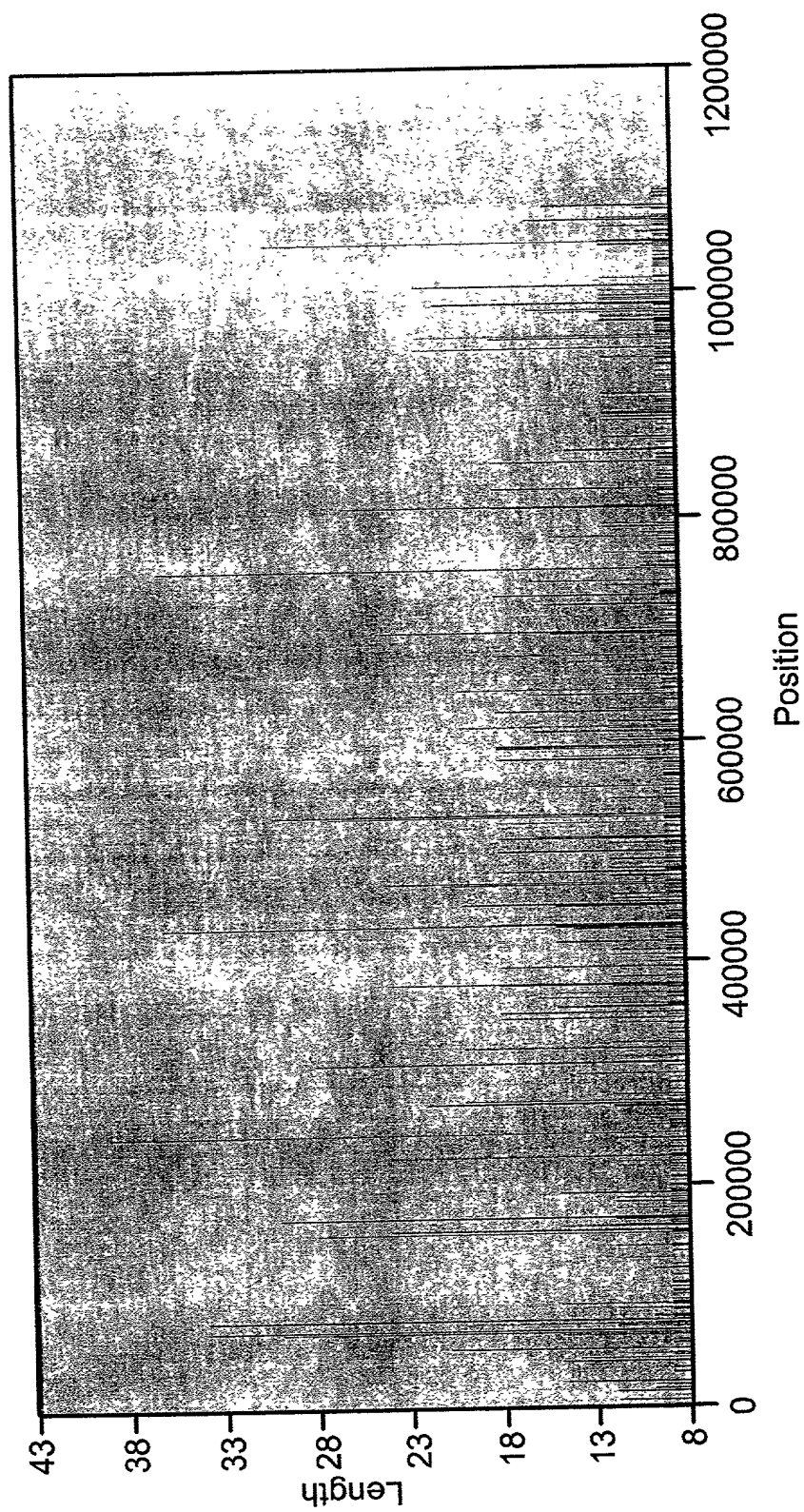
Fig. 1d
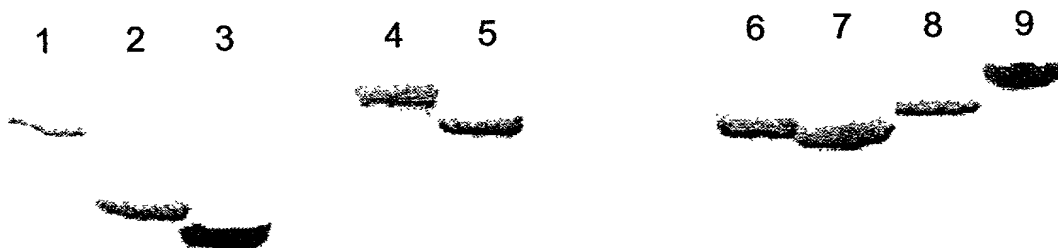
Fig. 2

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                     1                                                  50
Ec K12, DH5α        ~~~GTTATGT CTTATCCCAC GGTATTTAAT ATGGTTCATT AGGATGTTTA 25*
Ec Bsr9b            ~TTGTTATGT CTTATCCCAC GGTATTTAAT ATAGTTCATT TGGATGTTCA 26*
Ec Bsr9c            TTTGTTATGT CTTATCCCAC GGTATTTAAT ATAGTTCATT TGGATGTTCA 27*
Ec ETEC             ~TCTATGTTC TTATCNCCAC GGTNTTTAAT ATGGTtCATT AGGATGTTTA 28*

        Consensus   -----T-T-- -T---CCCAC GGTATTTAAT AT-GTTCATT -GGATGTT-A 29*

                     51                                                 100
Ec K12, DH5α        TTTCTTGATT TTGCATATGA GTATATTA.. CCCCCCCCTC AAAAAAATAA
Ec Bsr9b            TTTCTTTATT TTGCATATGA GTATATTA.. ....CCCCTT CAAAAAATAA
Ec Bsr9c            TTTCTTTATT TTGCATATGA GTATATTA.. ....CCCCTT CAAAAAATAA
Ec ETEC             TTTCTTGATT TTGCATATGA GTATATTACC CCCCCCCCTC AAAAAAATAA

        Consensus   TTTCTT-ATT TTGCATATGA GTATATTA-- ----CCCCT- -AAAAAATAA

                     101                                                150
Ec K12, DH5α        ATTAATTAAA ATGATGGCTT ATATAAAATA AAATTTAAAG CAAGGAATCT
Ec Bsr9b            ATTAATTAAA ACGATTGCTT ATATAAAACA AAATTTAAAG CAAGGAATCT
Ec Bsr9c            ATTAATTAAA ACGATTGCTT ATATAAAACA AAATTTAAAG CAAGGAATCT
Ec ETEC             ATTAATTAAA ATGATGGCTT ATATNAAATA NAATTTAAAG CAAGGANTCT

        Consensus   ATTAATTAAA A-GAT-GCTT ATATAAAA-A AAATTTAAAG CAAGGAATCT

                     151                                                200
Ec K12, DH5α        CAATGGATGT TAAACAAAAT GAGATTTTGT GAAAGCAATA AATTATTGAC
Ec Bsr9b            CAATGGATGT TAAACAAAAT GAGATTTAGT GAAAACAATA AATTATTCAC
Ec Bsr9c            CAATGGATGT TAAACAAAAT GAGATTTAGT GAAAACAATA AATTATTCAC
Ec ETEC             CAATGGATGT TAAACANAAT GAGATTTTGT GAANGCNATN NATTATTGNC

        Consensus   CAATGGATGT TAAACAAAAT GAGATTT-GT GAAA-CAATA AATTATT-AC

                     201                                                250
Ec K12, DH5α        TTCGTTTTAG ATTTGTTTAG CTATAATGTT ATACATTCAA ATGACTGAAC
Ec Bsr9b            TTCGTTTTAG ATTTGTTTAG CTATAATGTT ATACATTCAA ATGACTGAAC
Ec Bsr9c            TTCGTTTTAG ATTTGTTTAG CTATAATGTT ATACNATTCAA ATGACTGAAC
Ec ETEC             TTCGTTGTAN ATTTGCTNAG CTATAATGTT ATNCATTCAA ATGACTGAAC

        Consensus   TTCGTT-TAG ATTTG-TTAG CTATAATGTT ATACATTCAA ATGACTGAAC

                     251       264
Ec K12  DH5α        ATCCTGTAAT TAAA
Ec Bsr9b            ATCCTGTATT TAA-
Ec Bsr9c            ATCCTGTAAT TAA-
Ec ETEC             ATCCTGTNNT TANA

        Consensus   ATCCTGTAAT TAA-
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* SEQ ID NO

Fig. 3a

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                     1                                                   50
Ec K12, DH5α         TTTNCCCGGA AAAAAATAGG AAAGGGGGGG GGGCTAATCG GCAGGGAAGG 30*
Ec K12, w3110        TNTTNNNCGG AAAAAAATNG AAAGGGGGGG GGGCTAATCG GCAGGGAAGG 31*
Ec Bsr9c             ~~TTTNCCGG AAAAAAATNG AAA..GGGGG GGGCTAATCG GCAGGGAAGG 32*
Ec (wt) 1            ~~TNTNCGGA AAAAAANAGG AAAGGGGGGG GGGCTAATCG GCAGGGAAGG 33*
Ec (wt) 54           ~~~~~~~NCG GAAAAAAATG AAA.GGGGGG GGGCTAATCG GCAGGGAAGG 34*
Ec (wt) 68           ~~~~~~~~CG GAAAAAAATG AAA.GGGGGG GGGCTAATCG GCAGGGAAGG 35*

        Consensus    ---------- -AAAAAA--G AAA--GGGGG GGGCTAATCG GCAGGGAAGG 36*


                     51                                                  100
Ec K12, DH5α         CCGCCCCGGA TAGCGGGCGG CANAAGGAAT CANAATTTCC AGGTCAGACG
Ec K12, w3110        CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGACG
Ec Bsr9c             CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGATG
Ec (wt) 1            CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGACG
Ec (wt) 54           CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGATG
Ec (wt) 68           CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGATG

        Consensus    CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGA-G


                     101                                                 150
Ec K12,DH5α          GGCTGCAAGT TGCAGACCGT TAAAATCATC GGNNGGGGTG TCGTACCACA
Ec K12, w3110        GGCTGCAAGT TGCAGACCGT TAAAATCATC GGTTGGGGTG TCGTACCACA
Ec Bsr9c             GGCTGCAAGT TGCAGACCGT TATAATCATC GGTTGGGGTG TCGTACCACA
Ec (wt) 1            GGCTGCAAGT TGCAGACCGT TAAAATCATC GGTTGGGGTG TCGTACCACA
Ec (wt) 54           GGCTGCAAGT TGCAGACCGT TATAATCATC GGTTGGGGTG TCGTACCACA
Ec (wt) 68           GGCTGCAAGT TGCAGACCGT TATAATCATC GGTTGGGGTG TCGTACCACA

        Consensus    GGCTGCAAGT TGCAGACCGT TA-AATCATC GGTTGGGGTG TCGTACCACA


                     151                      180
Ec K12, DH5α         CTTTACCTGC CGTCAGCCCG AGATTAA-GTT ~G
Ec K12, w3110        CTTTACCTGC CGTCAGCCCG AGATTAA-GTT ~G
Ec Bsr9c             CTTTACCTGC CGTCAGCCCG AGATTAA~GTT ~G
Ec (wt) 1            CTTTACCTGC CGTCAGCCCG AGATTAAAGTT TGG
Ec (wt) 54           CTTTACCTGC CGTCAGCCCG AGAT~AAAGTT TGG
Ec (wt) 68           CTTTACCTGC CGTCAGCCCG AGAT~AAAGTT TGG

        Consensus    CTTTACCTGC CGTCAGCCCG AGAT-AA-GTT -G


* SEQ ID NO
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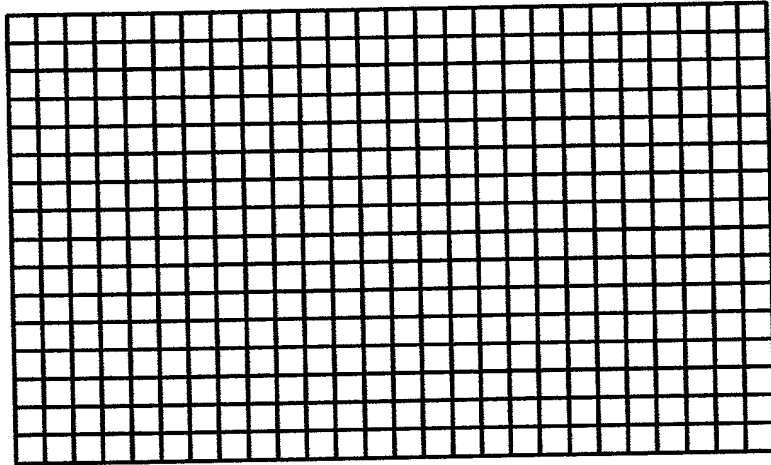
Fig. 3b

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Fig. 4